



Figure 1

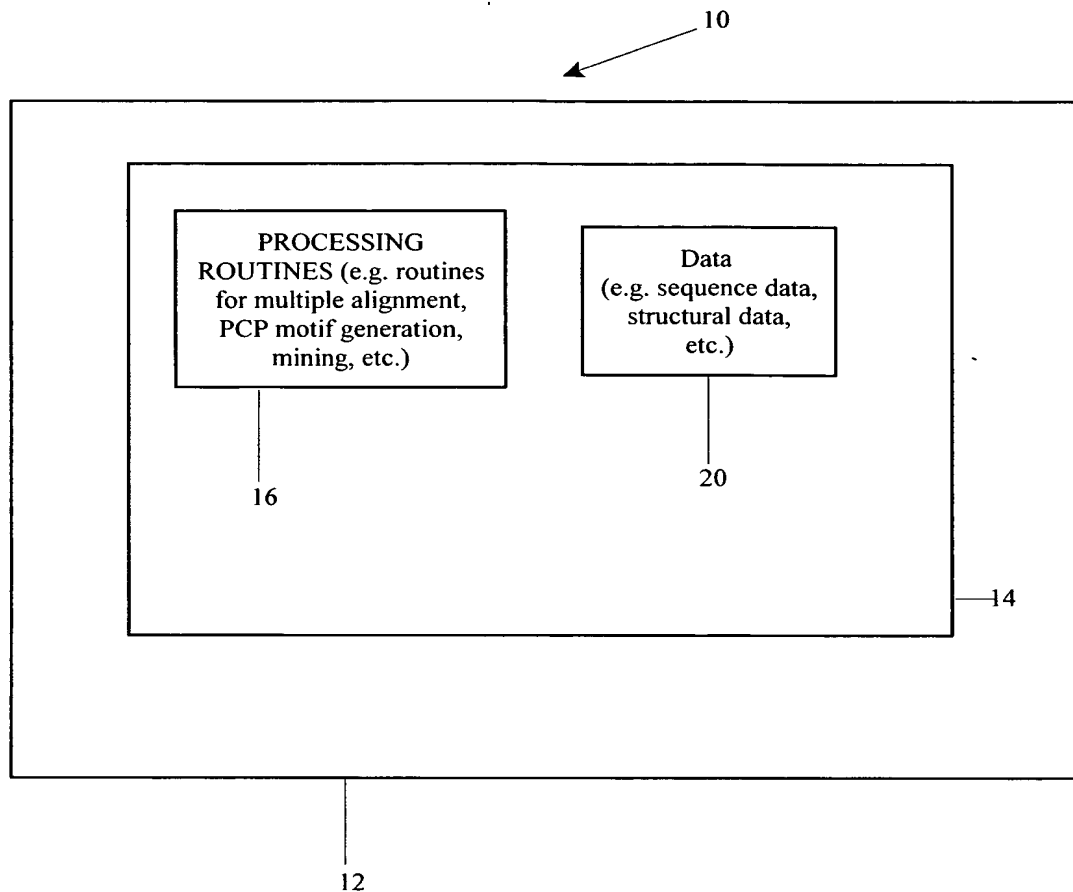


Figure 2

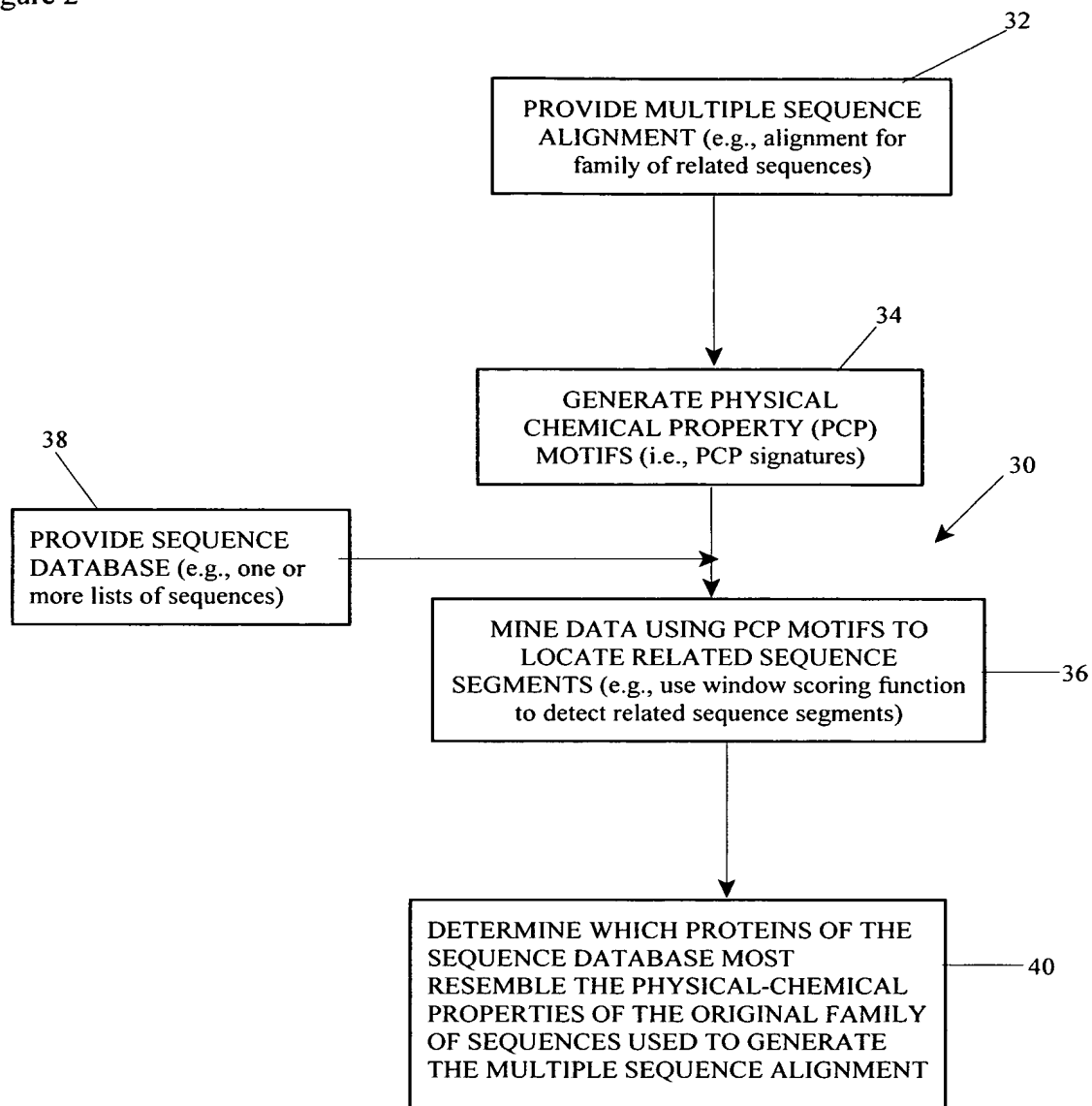


Figure 3

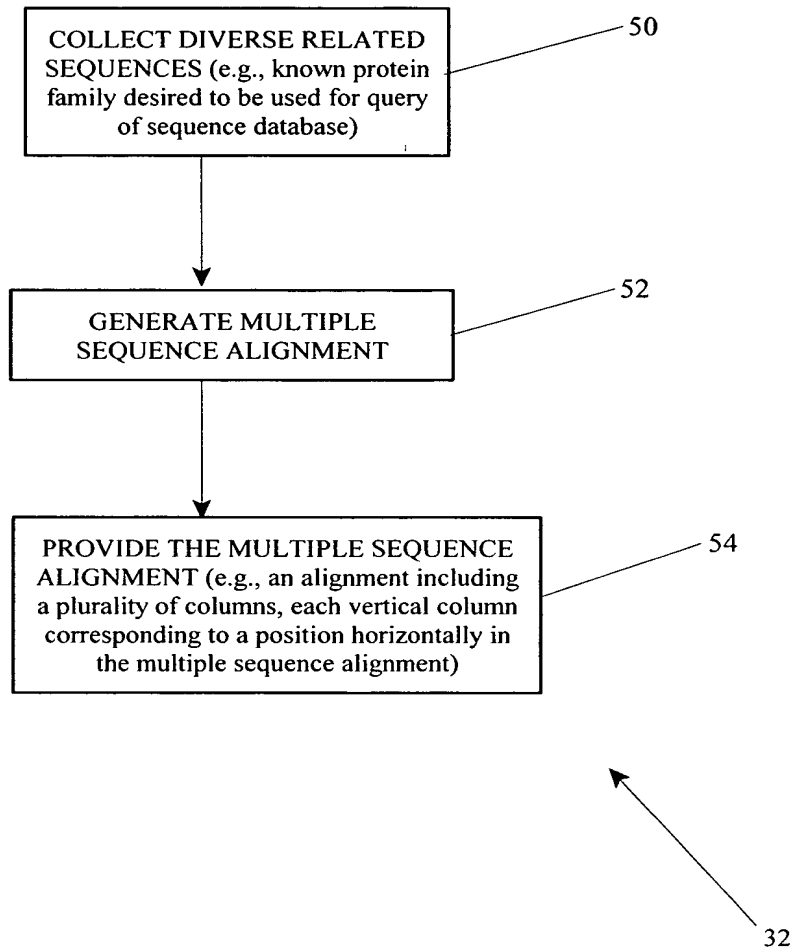


Figure 4

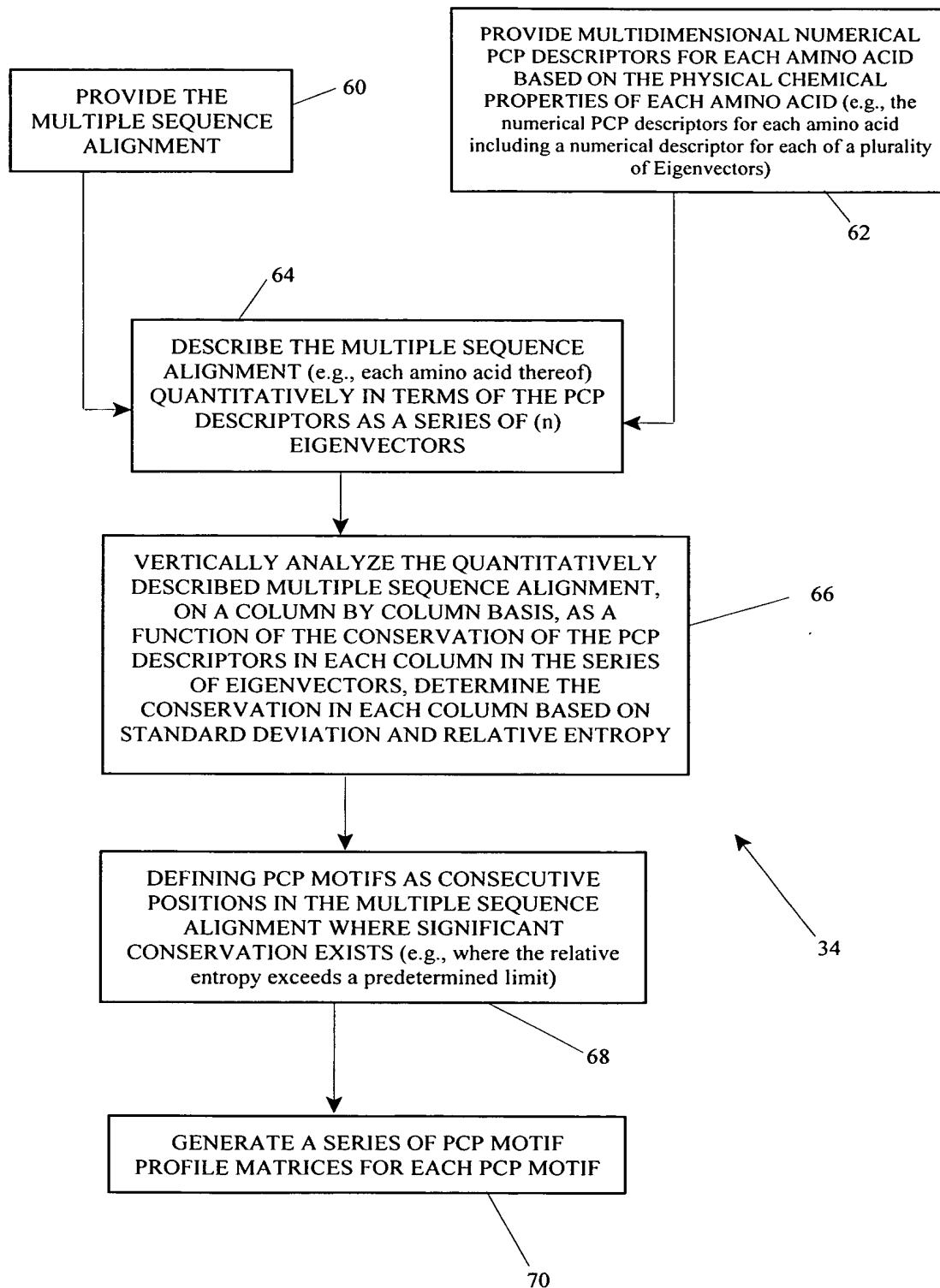


Figure 5

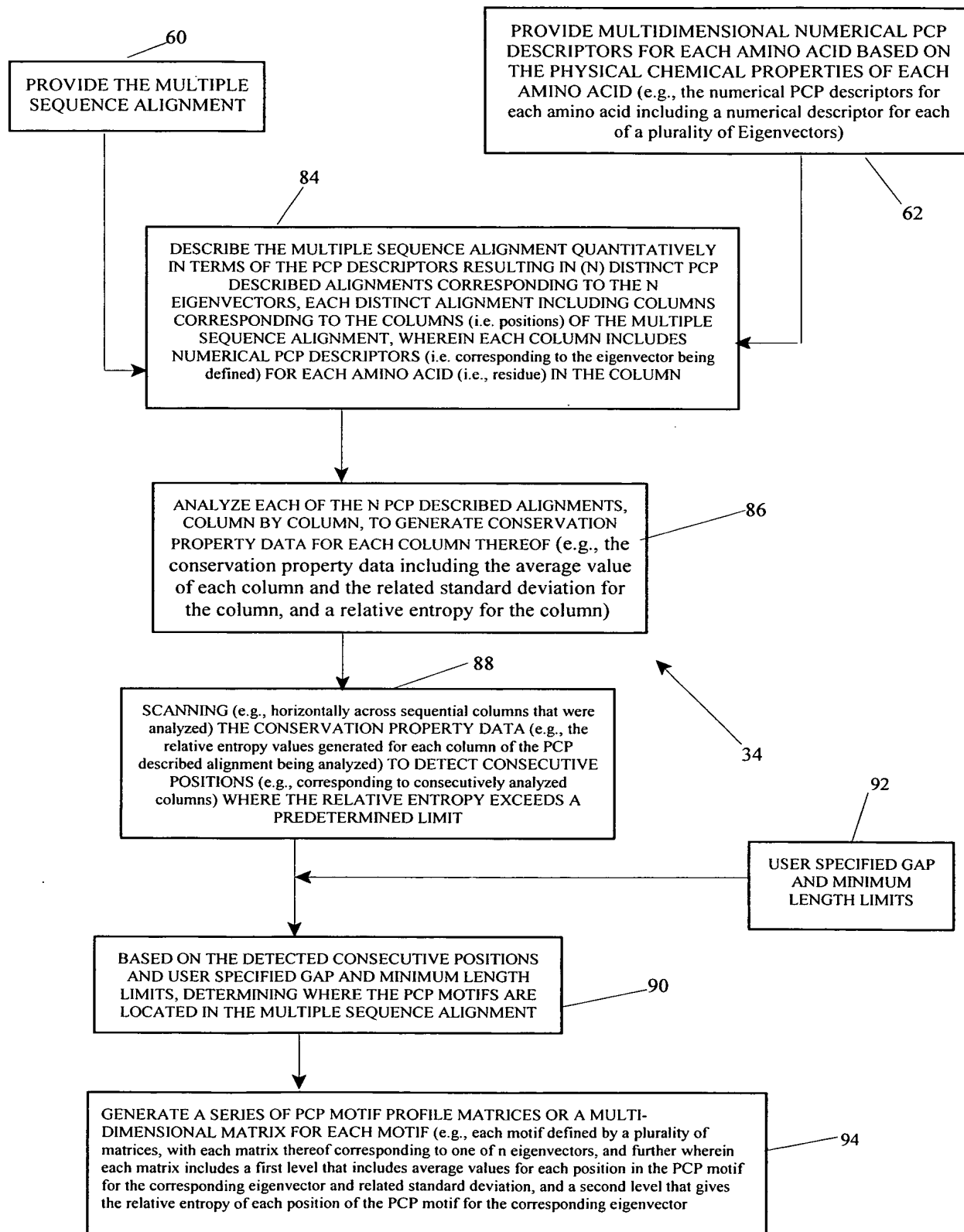


Figure 6

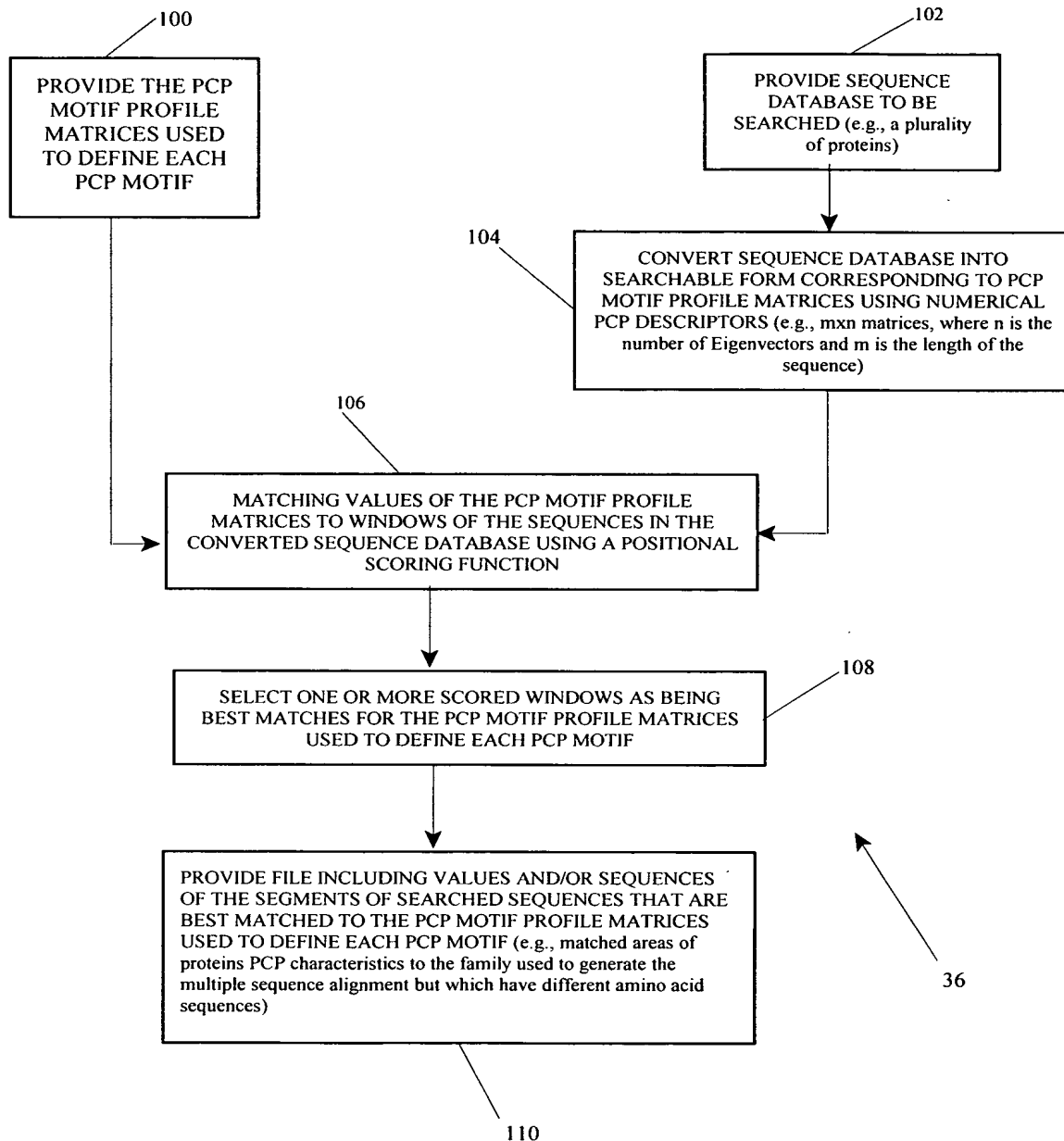


Figure 7

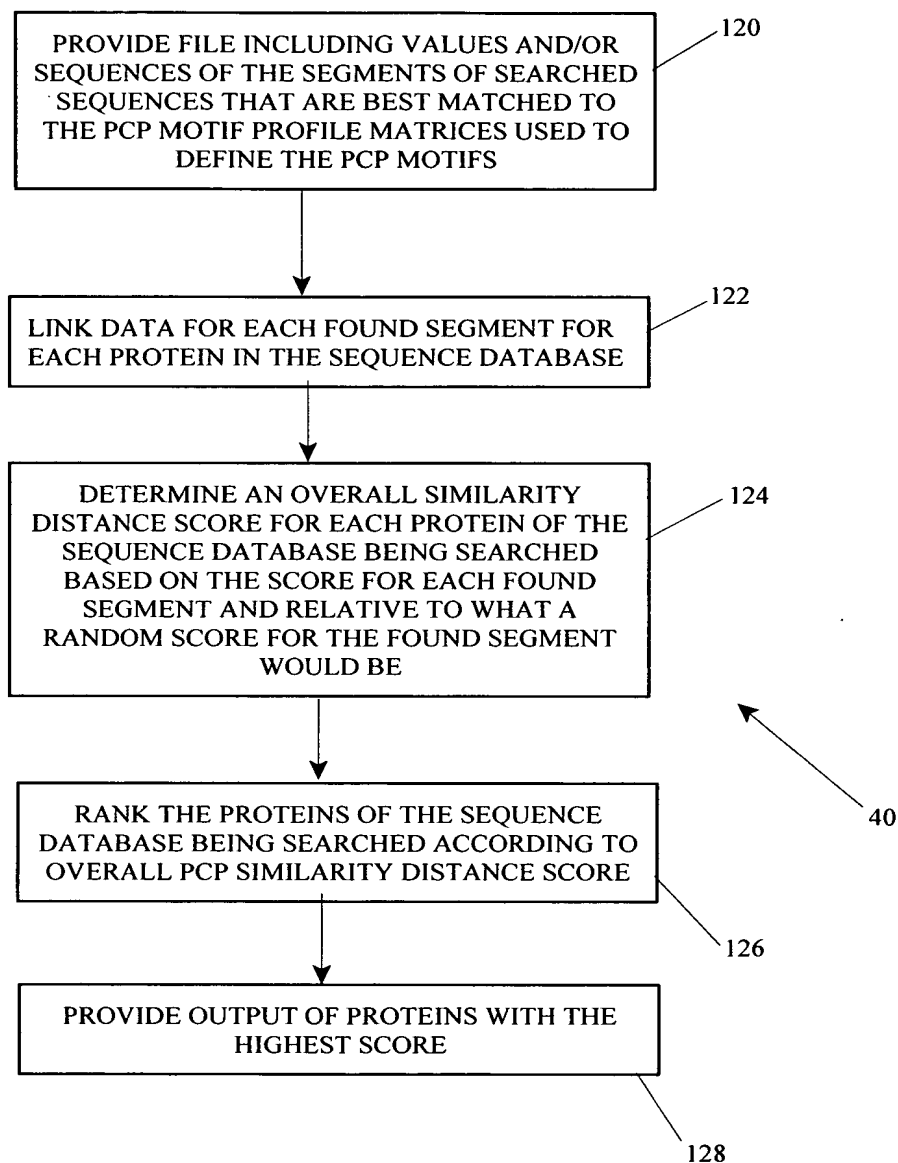


Figure 8

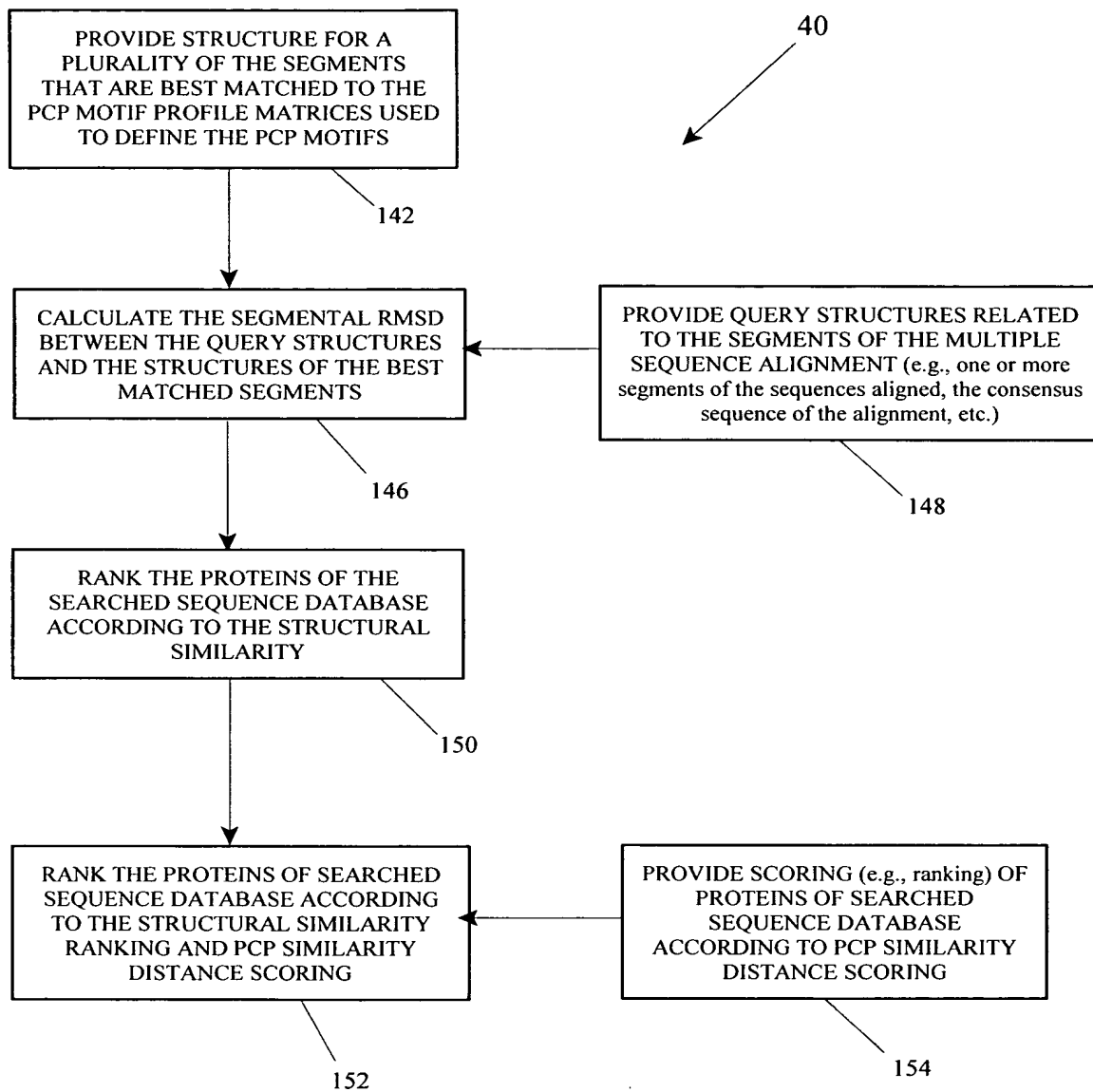


Figure 9A

Motif No.	Query sequence (human APE)	(S1)	(S2)	(S3)	(S4)	42 APE score ave. \pm std. dev	ASTRAL40 ave. \pm std. dev
1	62LKICSWNVVDGLRA 74	0.91*	0.90*	0.63*	0.73*	0.87 \pm 0.05	0.56 \pm 0.05
2	89PDILCLQETK 98	0.96*	0.93*	0.84*	0.70*	0.92 \pm 0.04	0.61 \pm 0.07
3	125 KEGYSGVGLLSRQCP 139	0.91*	0.86*	0.60	0.66	0.85 \pm 0.06	0.64 \pm 0.05
4	145 GIGDEEHDQEGRVIVAEFDSFVL 169	0.94*	0.77*	0.71	0.81	0.84 \pm 0.09	0.67 \pm 0.07
5	171 YVPNA 175	0.96*	0.96*	0.68	0.86	0.94 \pm 0.06	0.68 \pm 0.13
6	181 RLEYRQRW 188	0.80*	0.70*	0.78	0.77	0.74 \pm 0.06	0.67 \pm 0.05
7	204 PLVLCGDLNVAH 215	0.96*	0.88*	0.82*	0.78*	0.90 \pm 0.04	0.55 \pm 0.08
8	231 GFTPQERQFGEL 243	0.96*	0.91*	0.78	0.73	0.87 \pm 0.09	0.70 \pm 0.07
9	247 VPLADSF 254	0.96*	0.93*	0.70	0.83	0.91 \pm 0.08	0.74 \pm 0.11
10	264 YTFWTYM 270	0.86*	0.77*	0.61	0.70	0.84 \pm 0.08	0.61 \pm 0.06
11	274 RSKNVGWRLDYFLLSHSL 291	0.92*	0.89*	0.56	0.64	0.90 \pm 0.04	0.54 \pm 0.07
12	306 GSDHCPI 312	0.93*	0.94*	0.88*	0.83*	0.92 \pm 0.03	0.52 \pm 0.09

REPLACEMENT SHEET

Figure 9B

PDB ¹	Score in bits (fraction to the highest score)	Motifs found	SCOP ²	EC ³	Description
1HD7	1942 (1.00)	1,2,3,4,5,6,7,8,9,10,11,12	d.151.1.1	4.2.99.18	APE
1AKO	1861 (0.96)	1,2,3,4,5,7,8,9,10,11,12	d.151.1.1	3.1.11.2	Exonuclease III
2DNJ	1094 (0.56)	2,6,7,12	d.151.1.1	0.0.0.0	Deoxyribonuclease I
119Y	1056 (0.54)	1,4,5,6,7,9,12	d.151.1.2	0.0.0.0	Phosphatidylinositol phosphate Synaptotjanin
1B3U	840 (0.43)	5,7,9,12	a.118.1.2	0.0.0.0	Regulatory domain of protein phosphatase
1MDA	814 (0.42)	6,9,11,12	b.69.2.1	1.4.99.3	Methylamine dehydrogenase
1MPY	797 (0.41)	7,9,12	d.32.1.3	1.13.11.2	Catechol 2,3-dioxygenase
1EKM	792 (0.41)	6,7,12	b.30.2.1	1.4.3.6	Copper amine oxidase
1YRG	737 (0.38)	2,9,12	c.10.1.2	0.0.0.0	GTPase RNA1
1QQ9	698 (0.36)	5,6,12	c.56.5.4	3.4.11.-	Aminopeptidase

¹PDB code of the protein

²SCOP code and d.151.1 is the DNaseI superfamily code

³Enzyme commission classification number

Figure 9C

PDB ¹	Score in bits (fraction to the highest score)	MOLEGOS found	SCOP ²	EC ³	Description
1HD7	1942 (1.00)	1,2,3,4,5,6,7,8,9,10,11,12	d.151.1.1	4.2.99.18	APE (Mn/Mg/Pb)
1AKO	1831 (0.94)	1,2,3,5,6,7,8,9,10,11,12	d.151.1.1	3.1.11.2	Exonuclease III
2DNJ	1072 (0.55)	1,2,5,6,7,9,10,12	d.151.1.1	3.1.21.1	Deoxyribonuclease I
1I9Y	971 (0.50)	1,2,5,6,7,9,10,12	d.151.1.2		Phosphatidylinositol phosphate Synaptotjanin
1QQ9	698 (0.36)	5,6,9,10,12	c.56.5.4	3.4.11.-	Aminopeptidase (Zn, Ca)
1ATL	633 (0.33)	5,6,9,10,12	d.92.1.9	3.4.24.42	Snake venom metalloprotease (Zn, Ca)
1D09	619 (0.32)	5,9,12	d.58.2.1	2.1.3.2	Aspartate carbamoyltransferase (Zn)
1D2N	613 (0.32)	5,6,8,9,12	c.37.1.13		N-ethylmaleimide of sensitive fusion protein (Mg)
1D0B	579 (0.30)	2,5,9,12	c.10.2.1		InternalinB LRR domain (Ca)
1EEM	571 (0.29)	5,6,8,12	a.45.1.1		Glutathione S-transferase

¹PDB code of the protein

²SCOP code and d.151.1 is the DNaseI superfamily code

³Enzyme commission classification number

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Figure 10 - E1

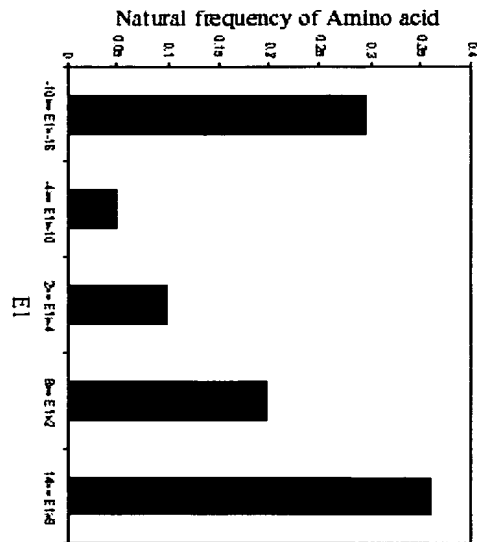


Figure 10 - E2

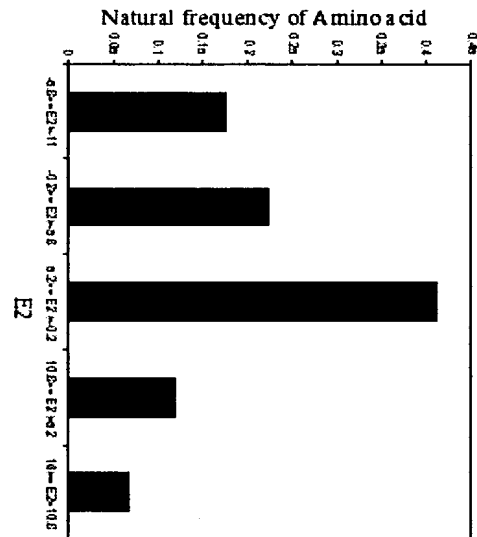


Figure 10 - E3

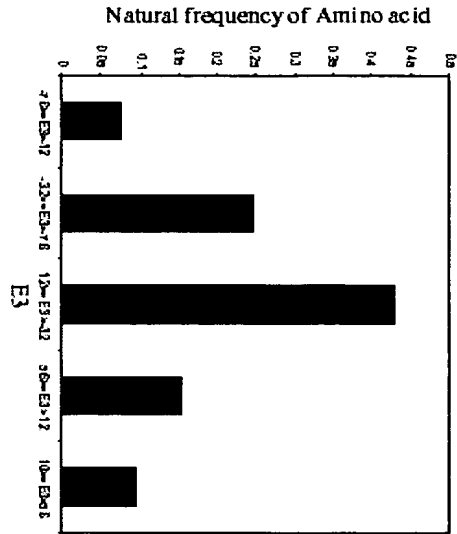


Figure 10 - E4

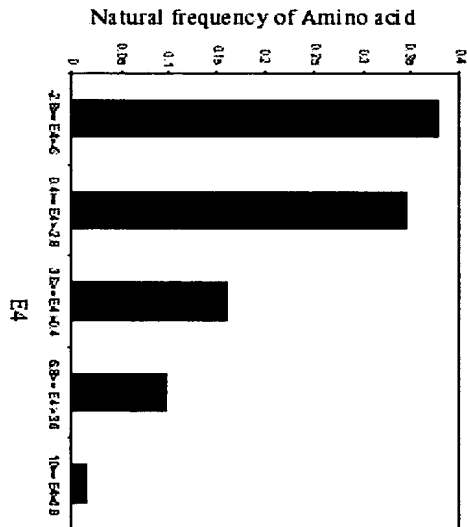


Figure 11

SEQ ID NO: 1	P	D	I	L	C	L	Q	E	T	K
E1	*	+	-	-	-	-	+	+	*	*
E2	*	-	*	*	*	*	-	-	*	-
E3	+	*	*	*	*	*	*	-	*	*
E4	*	+	*	*	+	*	+	+	*	-
E5	*	+	*	*	*	*	-	+	*	-

Figure 12A

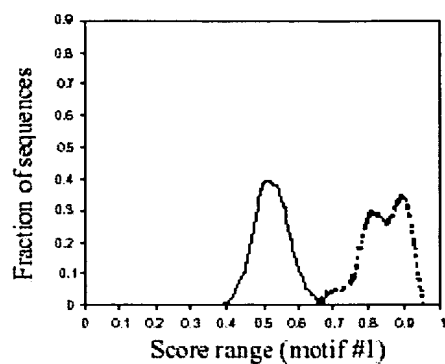


Figure 12B

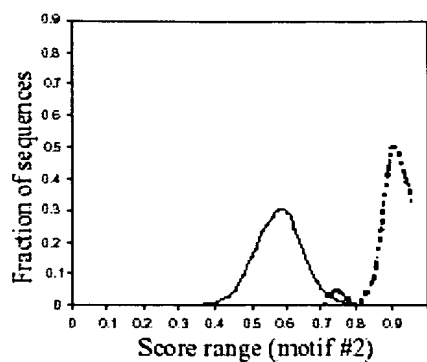


Figure 12C

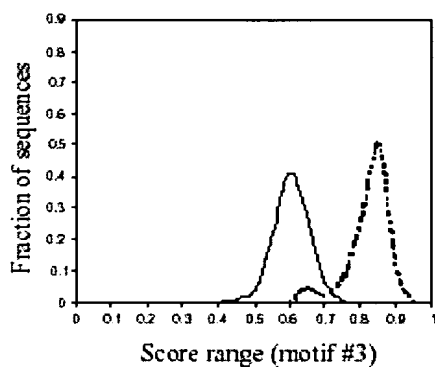


Figure 12D

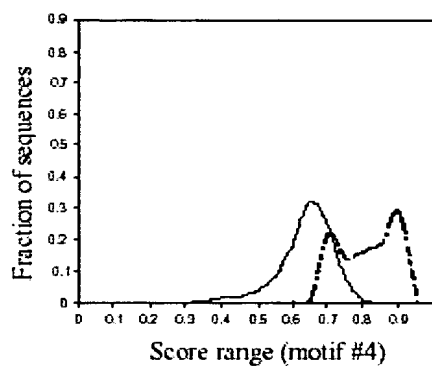


Figure 12E

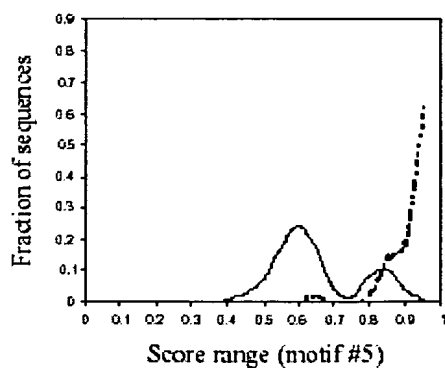


Figure 12F

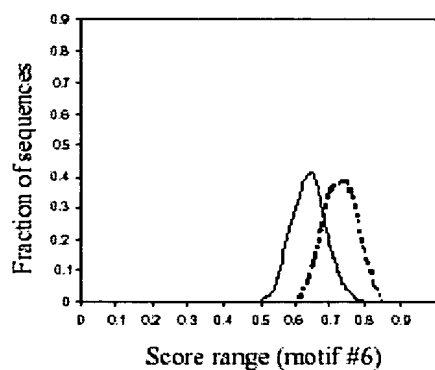


Figure 12G

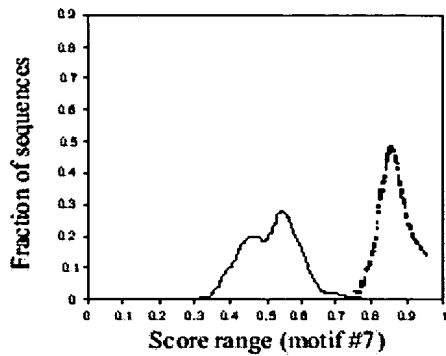


Figure 12H

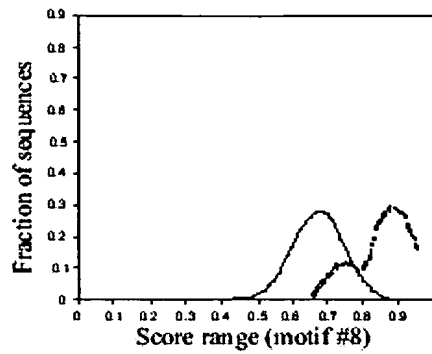


Figure 12I

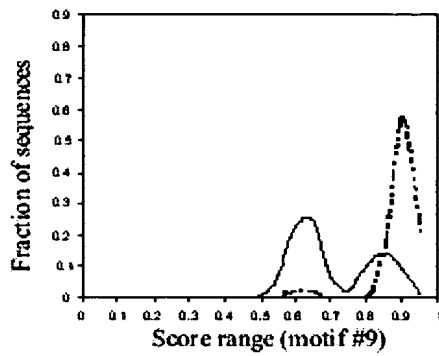


Figure 12J

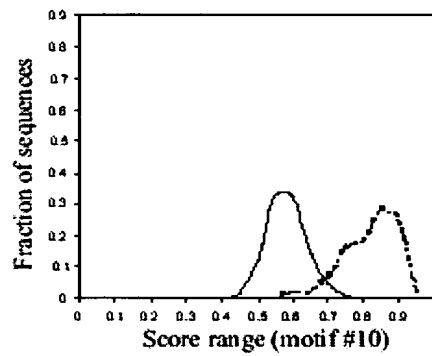


Figure 12K

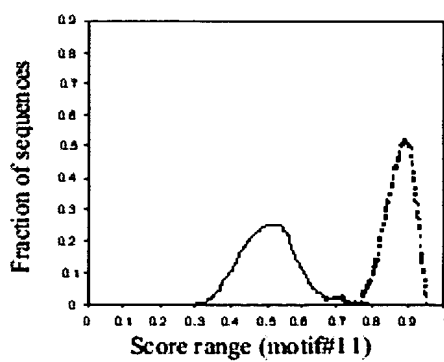
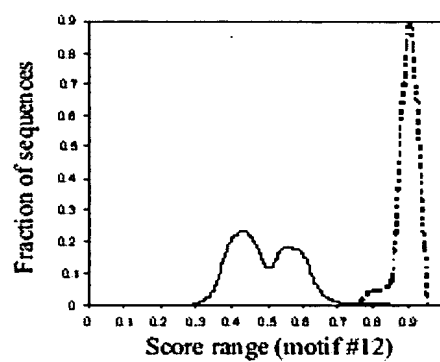


Figure 12L



REPLACEMENT SHEET

Figure 13

Seq ID No: 2	lbixLYEDPPDQKTSPSGKPAT	<u>1</u>	<u>LKICSWNVDGLRAW</u>IKKKGLDWVKE.EA
Seq ID No: 3	lako		<u>MKEVVSFNINGLRAR</u>P..HOLEAIVEkHQ
Seq ID No: 4	3dni		<u>LKIAAFNIRTFGe</u>	tksnatLASIVIRIVR...R
Seq ID No: 5	li9yA	ydpiheyvnhelrkrenefseHKNVK		<u>IFVASYNLNG..CS</u>ATTK.LENWLF.Pe

		<u>2</u>			
1bix		<u>P.....DILCLOETK</u>CSENKL.P..AELQELPGLSHQYWS.APSD	
1ako		<u>P.....DVIGLQETK</u>VHDDMF.P.lEEVAKLG..YNVfYH.G...	
3dni		<u>Y.....DIVLIQEV</u>DSHLVAvG..KLLDYLnqddpNTYH.YVVS	PLGR
li9yA		<u>ntpladiYVVGFOEIV</u>	qltsADPAkrreweSCVKRLl	ngkctsgpgYVQLRSGQL.V...	

		<u>3</u>		<u>4</u>	
1bix		<u>KEGYSGVGLLSR...QCP</u>LKVSYGIGDE....EHDQE	<u>GRVIVAEFD</u>
1ako		<u>QKGHYGVALLTK...ETP</u>IAVRGFPGD....DEEAq	<u>RRIIMAEIP</u>	...sl
3dni		<u>nSYKERYLFLFRpnkVSV</u>LDTYQ.YDDGccgnDSFSR	..EPAVVKFSshstk	
li9yA		<u>.....GTALMIF...Ckesclpsikn</u>	VEGTVKK.....tGLGN	KGAVAIRFD...ye	

		<u>5</u>		<u>6</u>	
1bix		<u>..SFVLVTAYVPNAGRGLV..RLEYRQRWDEAFRKF</u>	FLKG.....LA...S.RK.	<u>PLVL</u>	
1ako		<u>lgNVTVINGYFPQGESRDHpiK</u>	PAKAQFYQNLQNYLET.....EL...KrDN	<u>PVLI</u>	
3dni		<u>vkEFAIVALHSAPS</u>DAVAEINSLYDVYLDVQqkwh.LN	DVMI
li9yA		<u>dtGLCFITSHLAAGY</u>TNYDERDHDYRTIASgl	rfrgrSI...F.NHd	<u>YVW</u>

		<u>7</u>		<u>8</u>	
1bix		<u>CGDLNVAHEEIDLRN</u>PKGKN..KNAGFTPOEROGF	
1ako		<u>MGDMNIS</u>	TDLDIGIgeenRKRWLrtGKCSFLPEEREWM	
3dni		<u>MGDFNAD</u>CSYVTSSQWSS	
li9yA		<u>FGDFNY</u>RISLtyeevvp	ciaqgklsylfeydqLNKQM	

		<u>9</u>		<u>10</u>		<u>11</u>
1bix		<u>G..ELLQAVPLADSEFRHLYPNT</u>	TPYAYTFWTY..MMNARSKNV...GWRLDYFLLSHS	..LL		
1ako		<u>D..RLMSW.GLVD</u>	TFRHPQTADRFSWFDY..RSKGFDDNR...GLRIDLLLASQP	..LA		
3dni		<u>I..RLRTSSTFQWLIP</u>dSADTTATST...NCAYDRIVVAGS	lIQ	
li9yA		<u>LtgKVFP..FFSELPI</u>tfPPTYKFDigTDIYDTSdkhrv	PAWTDRILYRGE.L		

				<u>12</u>	
1bix		PALC..DSKIRSKAL....	<u>GSDHCPT</u>	ITLYLAL
1ako		ECCV..ETGIDYEIRsmek	<u>PSDHAPV</u>	WATFRR
3dni		SSVVpgSAAPFDFQaayglsnemalA	<u>ISDHYPVEVTLT</u>	
li9yA		.VPH..SYQSV.PLY....	<u>YSDHRPT</u>	IYATYEAnivkvdrekakilfeel

1bix
1ako
3dni
li9yA	ynqrkqevrdsq

Figure 14

